

16 Jun 2005

## Alignment Results

Alignment: Global Protein alignment against reference molecule  
Parameters: Scoring matrix: BLOSUM 62

Reference molecule: SEQIDNO:2, Region 1-313

Number of sequences to align: 2

Settings: Similarity significance value cutoff:  $\geq 60\%$ 

## Summary of Percent Matches:

Reference:	SEQIDNO:2	1 -	313	(	313 aa)	--
Sequence 2:	SEQIDNO:24	1 -	288	(	288 aa)	89%

SEQIDNO:2	1	MSSSNWIDDAFTEEELLAIDAIEASYNFSRSSSSSSSAAPTQATTSVHGHEEDPNQIPN
SEQIDNO:24	1	.....
SEQIDNO:2	61	NIRRLPRSITSSTSYKRFPLSRCRARNFPAMRFGGRILYSKTATEVDKRAMQLIKVLDT
SEQIDNO:24	61	.....
SEQIDNO:2	121	KRDESGIAFVGLDIEWRPSFRKGVLPQKQVATVQICVDSNYCDVMHIFHSGIPQSLQHLIE
SEQIDNO:24	121	.....
SEQIDNO:2	181	DSTLVKVGIGIDGDSVKLFHDYGVSIKDVEDLSDLANQKIGGDKKWGLASLTETLVCKEL
SEQIDNO:24	181	.....
SEQIDNO:2	241	LKPNRIRLGNWEFYPLSKQQLQYAATDAYASWHLYKVTTTKNHLTLNDLEAKISHRSNY
SEQIDNO:24	241	.....-----K..PDAV.GS---
SEQIDNO:2	301	NTVTCRKPGGYLR
SEQIDNO:24	289	-----

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Pos	Sequence	Start	End	Length	Matches	%Matches
Ref 1	SEQIDNO:2	1	313	313 aa		
2	SEQIDNO:24	1	288	288 aa	281	89